



SEQUENCE LISTING

<110> Zeneca Limited

<120> Insecticidal Proteins from Paecilomyces and Synergistic Combinations Thereof

<130> SYN-128

<140> US 10/019,823

<141> 2001-12-21

<150> PCT/GB00/02457

<151> 2000-06-23

<150> GB 9915215.9

<151> 1999-06-29

<150> GB 9930536.9

<151> 1999-12-23

<160> 65

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 33

<212> PRT

<213> Paecilomyces sp.

<220>

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 1

Xaa Xaa Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
1 5 10 15

Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
20 25 30

Arg

<210> 2

<211> 33

<212> PRT

<213> Paecilomyces sp.

<400> 2

Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala Leu Pro
1 5 10 15

Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys Val Cys
20 25 30

Arg

<210> 3

<211> 35

<212> PRT
<213> Paecilomyces sp.

<220>
<221> VARIANT
<222> 1, 2
<223> Xaa = Any Amino Acid

<400> 3
Xaa Xaa Gly Lys Ile Cys Thr Pro Ala Gly Val Lys Cys Pro Ala Ala
1 5 10 15
Leu Pro Cys Cys Pro Gly Leu Arg Cys Ile Gly Gly Val Asn Asn Lys
20 25 30
Val Cys Arg
35

<210> 4
<211> 332
<212> DNA
<213> Paecilomyces sp.

<400> 4
ggcaagatct gcactcctgc tggagttgta cgtatttca tccatttcct ycaccactcc 60
tctaacatga agcaacttcc tcttctctct agaaatgtcc cgccgctctt cttgtgtgcc 120
ccggacttcg ctgcatacgcc ggcgtcaacg taagtaccca tggatctggc aagcgagacc 180
ataacatgac gcagtataact aaccctggcc gttagaacaac aaggttgtga gtcgacatgt 240
tktacaacct ctacaaacgcg gcgactaat gacaacggta gtgccggtaa ttcttagtgtc 300
gcaacttttgc agcgtggat aagtatgttt cg 332

<210> 5
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 5
gggaaaattt gtacgccccgc ggggggttgta cgtatttca tccatttcct ccaccactcc 60
tctaacatga agcaacttcc tcttctctct agaaatgtcc cgccgctctt cttgtgtgcc 120
ccggacttcg ctgcatacgcc ggcgtcaacg taagtaccca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa gttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgcgc aacttttag 300
cgtggataa gtatgtttcg 320

<210> 6
<211> 320
<212> DNA
<213> Paecilomyces sp.

<400> 6
gggaaaatct gtacgccccgc ggggggttgta cgtatttca tccatttcct ccaccactcc 60
tctaacatga agcaacttcc tcttctctct araaatgtcc cgccgctctt cttgtgtgcc 120
ccggacttcg ctgcatacgcc ggcgtcaacg taagtaccca tcctgacacg acgtgaaggc 180
aatgtactga ccctggccgt tatagaacaa gttgtgagt cgacatgttt tacaacctct 240
acaaacgcgc gcactaatga caacggtagt gccggtaatt ctagtgcgc aacttttag 300
cgtggataa gtatgtttcg 320

<210> 7
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide codon optimised

<400> 7
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg ccggcaagat ctgcaccccg gccggcgtga agtgcggcggc cgccctccccg 120
tgctgcccgg gcctccgctg catcggcggc gtgaacaaca aggtgtgccg ctga 174

<210> 8
<211> 174
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic polynucleotide codon optimised

<400> 8
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg ccggtaaaat ttgtaccccg gccggcgtga agtgcggcggc cgccctccccg 120
tgttgtccgg gcctcaggtg tattggtggt gtgaataata aagtgtgtcg ctga 174

<210> 9
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence containing intron sequence

<400> 9
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg ccggcaagat ctgcactcct gctggagttg ttttttctg cttctacctt 120
tgatatatat ataataatta tcattaatta gtagtaatat aatatttcaa atatttttt 180
caaaaataaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgtatatt 240
ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccg 300
gcttttcctt gctgccccgg acttcgctgc atcggcggcgt tcaacaacaa ggtttgccgg 360
taa 363

<210> 10
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 10
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg ctcctacgg caagatctgc actcctgctg gagttgtttg tttctgcttc 120
tacctttat atatatataa taattatcat taatttagtag taatataata tttcaaatat 180
ttttttcaaa ataaaaagaat gtagtatata gcaattgctt ttctgttagtt tataagtgtg 240
tatattttaa ttatataactt ttctaatata tgaccaaaac atggtgatgt ttagaaatgt 300
cccgccggctc ttcttgctg ccccgactt cgctgcacatcg gcggcgtcaa caacaagg 360
tgccggtaa 369

<210> 11
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
 <223> Synthetic sequence

 <400> 11
 atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
 gagatccagg cctcctacat ctgcactcct gctggagttg tttgtttctg cttctacatt 120
 tgatatataat ataataatta tcattaatta gtagtaatataat aatatttcaa atattttttt 180
 caaaataaaaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgttatatt 240
 ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa atgtcccccg 300
 gctttccctt gctgccccgg acttcgctgc atcggcggcg tcaacaacaa ggtttgcgg 360
 taa 363

<210> 12
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic sequence containing intron and codon optimised

<400> 12
 atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
 gagatccagg ccggcaagat ctgcaccccg gccggcgtgg tttgtttctg cttctacatt 120
 tgatatataat ataataatta tcattaatta gtagtaatataat aatatttcaa atattttttt 180
 caaaataaaaaa gaatgttagta tatagcaatt gctttctgt agtttataag tgtgttatatt 240
 ttaatttata acttttctaa tatatgacca aaacatggtg atgttttagaa gtgcccggcc 300
 gcccctccgt gctgccccgg cctccgctgc atcggcggcg tgaacaacaa ggtgtgccgc 360
 tga 363

<210> 13
 <211> 439
 <212> DNA
 <213> Paecilomyces sp.

<400> 13
 tctacttctt catctcacgc catatatcct cccaaaatca cacctttcc ttcaccatgc 60
 aaatctccgc cgtcattgtc gcactcttcg ccagcgccgc catggccggc aagatctgca 120
 ctcctgctgg agttgtacgt attttcatcc atttcctyca ccactcctct aacatgaagc 180
 aactttctct tctctctaga aatgtcccgcc ggctttcttct tgctgccccgg gacttcgctg 240
 catggcggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
 gtatactaactt cctggccgtt atagaacaag gttgtgagtc gacatgttkt acaacctcta 360
 caaacgcgcg cactaatgac aacggtagtg ccggtaattt tagtgcgc acttttgagc 420
 gtgggataag tatgcttcg 439

<210> 14
 <211> 102
 <212> DNA
 <213> Paecilomyces sp.

<400> 14
 ggcaagatct gcactcctgc tggagttaaa tgtcccgccg ctcttccttg ctgccccgg 60
 cttcgctgca tcggcggcgt caacaacaag gtttgcgg 102

<210> 15
 <211> 84
 <212> DNA
 <213> Dahlia sp.

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<400> 15
atggtaata gatctgtgc ttttctgct ttgttctta ttctttgt tttggctatt 60
tcagatattg cttctgttcc agga 84

<210> 16
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Radish signal sequence

<400> 16
atggctaagt ttgcttctat tattgctctt ttgttgctg cacttgttt gtttgctgca 60
tttgaagctc caactatggt tgaagct 87

<210> 17
<211> 72
<212> DNA
<213> Zea mays

<400> 17
atgggtggca gcggcagggc tgctctgctg ctggccctgg tggccgttag cctggccgtg 60
gagatccagg cc 72

<210> 18
<211> 90
<212> DNA
<213> Nicotiana sp.

<400> 18
atgggatttg ttctctttc acaattgcct tcatttcttc ttgtctctac acttctctta 60
ttcctagtaa tatcccactc ttgccgtgcc 90

<210> 19
<211> 51
<212> DNA
<213> Paecilomyces sp.

<400> 19
atgcaaatct ccgcccgtcat tgtcgcaactc ttgcgcagcg ccgcattggc c 51

<210> 20
<211> 28
<212> PRT
<213> Dahlia sp.

<400> 20
Met Val Asn Arg Ser Val Ala Phe Ser Ala Phe Val Leu Ile Leu Phe
 1           5           10          15
Val Leu Ala Ile Ser Asp Ile Ala Ser Val Ser Gly
 20          25

<210> 21
<211> 29
<212> PRT
<213> Artificial Sequence

<220>

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<223> Radish protein target sequence

<400> 21

Met Ala Lys Phe Ala Ser Ile Ile Ala Leu Leu Phe Ala Ala Leu Val
1 5 10 15
Leu Phe Ala Ala Phe Glu Ala Pro Thr Met Val Glu Ala
20 25

<210> 22

<211> 24
<212> PRT
<213> Zea Mays

<400> 22

Met Gly Gly Ser Gly Arg Ala Ala Leu Leu Leu Ala Leu Val Ala Val
1 5 10 15
Ser Leu Ala Val Glu Ile Gln Ala
20

<210> 23

<211> 30
<212> PRT
<213> Nicotiana sp.

<400> 23

Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
1 5 10 15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
20 25 30

<210> 24

<211> 17
<212> PRT
<213> Paecilomyces sp.

<400> 24

Met Gln Ile Ser Ala Val Ile Val Ala Leu Phe Ala Ser Ala Ala Met
1 5 10 15
Ala

<210> 25

<211> 44
<212> DNA
<213> Artificial Sequence

<220>

<223> Primers

<400> 25

tcgggctcgc atgaattcgc gccgcattt tttttttttt tttt 44

<210> 26

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 26
tcgggctcgc atgaattcg 19

<210> 27
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 27
atgaattcgc ggccgcatt 18

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 28
tcgggctcgc atgaattcgc g 21

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 29
ctcgcatgaa ttgcggccg c 21

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc feature
<222> 9, 12, 15
<223> n = A,T,C or G

<400> 30
athtgyacnc cngcngg 17

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primers

<221> misc_feature
<222> 9, 12, 15, 18
<223> n = A,T,C or G

<400> 31
athtgyacnc cngcnggngt 20

<210> 32
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 6, 9, 12, 15
<223> n = A,T,C or G

<400> 32
acnccngcng gngtnaa 17

<210> 33
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 12, 15
<223> n = A,T,C or G

<400> 33
ccntgytgyc cnggnyt 17

<210> 34
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 2, 14
<223> n = A,T,C or G

<400> 34
tnaartgyat hggngg 16

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primers

<221> misc_feature
<222> 3, 6, 18
<223> n = A,T,C or G

<400> 35
ggngtnaaya ayaargtntg 20

<210> 36
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 12, 15, 18, 21, 24
<223> n = inosine

<400> 36
aarathgya cnccngcngg ngttnaa 26

<210> 37
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 6, 9, 12, 21, 24
<223> n = inosine

<400> 37
ccngcnggng tnaartgycc ngcngc 26

<210> 38
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 6, 9, 12, 15, 18
<223> n = inosine

<400> 38
tgyccngcng cnytnccntg ytgycc 26

<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence

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<220>
<223> Primers

<221> misc_feature
<222> 9, 12, 15
<223> n = inosine

<400> 39
tgyathggng gngtnaayaa yaargt 26

<210> 40
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 40
taaatgtccc gcggctcttc c 21

<210> 41
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 41
cggctcttcc ttgctgcccc g 21

<210> 42
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 42
tgctgccccg gacttcgctg c 21

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 23, 24, 25, 26, 27
<223> n = A,T,C or G

<400> 43
ggtttaatta cccaaaggttt agnnnnnn 27

<210> 44
<211> 22

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<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 44
ctcaaacttg ggtaattaaa cc                                22

<210> 45
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 45
ggtttaatta cccaaagg                                         18

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 46
taattaccca agtttgag                                         18

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<400> 47
ggtttaatta cccaaaggttg ag                                22

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primers

<221> misc_feature
<222> 3, 15, 18, 21
<223> n = inosine

<400> 48
canacyttrt trttnacncc ncc                                23

<210> 49
<211> 21
<212> DNA

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<213> Artificial Sequence

<220>

<223> Primers

<400> 49
atgcagcgaa gtccggggca g 21

<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 50
ggggcagcaa ggaagagccg c 21

<210> 51

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 51
aagagccgcg ggacatttaa c 21

<210> 52

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 52
agttaaatgt cccgcggctc ttccttgctg ccccgactt cgctgcatac 49

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primers

<400> 53
gatgcagcga agtccggg 18

<210> 54

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN crylIal Embl. Accession No. X62821

<221> VARIANT

<222> 602

<223> Xaa = Any Amino Acid

<400> 54

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
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Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
20 25 30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
35 40 45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
50 55 60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65 70 75 80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
85 90 95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100 105 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115 120 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130 135 140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145 150 155 160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165 170 175
Ala Val Ser Gly Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
180 185 190
Ala Asn Leu His Leu Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
195 200 205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
210 215 220
Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
225 230 235 240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
245 250 255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
260 265 270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
275 280 285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
290 295 300
Pro His Pro Ser Phe Thr Ser Thr Trp Tyr Asn Asn Asn Ala Pro
305 310 315 320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
325 330 335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
340 345 350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355 360 365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370 375 380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385 390 395 400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405 410 415
Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile Ala
420 425 430
Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln Leu

435	440	445
Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro Asn		
450	455	460
Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser Ala		
465	470	475
Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala Asp		
485	490	495
Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu Val		
500	505	510
Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro Gly		
515	520	525
Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe Gly		
530	535	540
Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg Val		
545	550	555
Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser Ile		
565	570	575
Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn Arg		
580	585	590
Gly Glu Asp Leu Asp Tyr Lys Thr Phe Xaa Thr Val Gly Phe Thr Thr		
595	600	605
Pro Phe Ser Leu Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala Trp		
610	615	620
Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe Val		
625	630	635
Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala Gln		
645	650	655
Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu Lys		
660	665	670
Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val Glu		
675	680	685
Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe Glu		
690	695	700
Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met		
705	710	715

<210> 55
<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN cry1Ia2 Embl. Accession No. M98544

<400> 55			
Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala			
1	5	10	15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile			
20	25	30	
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr			
35	40	45	
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile			
50	55	60	
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly			
65	70	75	80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys			
85	90	95	
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile			
100	105	110	

Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
 355 360 365
 Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590

Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
 705 710 715

<210> 56
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN cry1Ia3 Embl. Accession No. L36338

<400> 56
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
 85 90 95
 Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
 100 105 110
 Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
 115 120 125
 Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
 130 135 140
 Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
 145 150 155 160
 Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
 165 170 175
 Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
 180 185 190
 Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
 195 200 205
 Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
 210 215 220
 Val Glu Arg Ala Gly Asp Tyr Ser Tyr His Cys Val Lys Trp Tyr Ser
 225 230 235 240
 Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val

260	265	270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr		
275	280	285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His		
290	295	300
Pro His Pro Ser Phe Thr Ser Thr Trp Tyr Asn Asn Asn Ala Pro		
305	310	315
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu		
325	330	335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser		
340	345	350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg		
355	360	365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr		
370	375	380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg		
385	390	395
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn		
405	410	415
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile		
420	425	430
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln		
435	440	445
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro		
450	455	460
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser		
465	470	475
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala		
485	490	495
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu		
500	505	510
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro		
515	520	525
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe		
530	535	540
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg		
545	550	555
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser		
565	570	575
Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn		
580	585	590
Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr		
595	600	605
Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala		
610	615	620
Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe		
625	630	635
Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala		
645	650	655
Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu		
660	665	670
Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val		
675	680	685
Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe		
690	695	700
Glu Ile Val Lys Tyr Ala Asn Glu Leu His Ile Glu Arg Asn Met		
705	710	715

<211> 719
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN cry1Ia4 Embl. Accession No. L49391

<400> 57

Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
1 5 10 15
Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
20 25 30
Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
35 40 45
Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
50 55 60
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
65 70 75 80
Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys
85 90 95
Gly Lys Asn Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile
100 105 110
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu
115 120 125
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser
130 135 140
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Ser
145 150 155 160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe
165 170 175
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala
180 185 190
Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys
195 200 205
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln
210 215 220
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser
225 230 235 240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg
245 250 255
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val
260 265 270
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr
275 280 285
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
290 295 300
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
305 310 315 320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu
325 330 335
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
340 345 350
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg
355 360 365
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr
370 375 380
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg
385 390 395 400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
405 410 415

Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Val Gly Ile Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Val Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Leu Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Lys Gln Leu His Ile Glu Arg Asn Met
 705 710 715

<210> 58
 <211> 719
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PROTEIN cry1Ia5 Embl. Accession No. Y08920

<400> 58
 Met Lys Leu Lys Asn Gln Asp Lys His Gln Ser Phe Ser Ser Asn Ala
 1 5 10 15
 Lys Val Asp Lys Ile Ser Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile
 20 25 30
 Glu Leu Gln Asn Ile Asn His Glu Asp Cys Leu Lys Met Ser Glu Tyr
 35 40 45
 Glu Asn Val Glu Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile
 50 55 60
 Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly
 65 70 75 80
 Gln Val Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys

	85	90	95
Gly Lys Asn Gln Trp Glu Ile Leu Phe Met Glu His Val Glu Glu Ile			
100	105	110	
Asn Gln Lys Ile Ser Thr Tyr Ala Arg Asn Lys Ala Leu Thr Asp Leu			
115	120	125	
Lys Gly Leu Gly Asp Ala Leu Ala Val Tyr His Asp Ser Leu Glu Ser			
130	135	140	
Trp Val Gly Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Arg Ser			
145	150	155	160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe			
165	170	175	
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala			
180	185	190	
Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys			
195	200	205	
Glu Trp Gly Leu Ser Ser Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln			
210	215	220	
Val Glu Arg Ala Gly Asp Tyr Ser Asp His Cys Val Lys Trp Tyr Ser			
225	230	235	240
Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Glu Ser Trp Val Arg			
245	250	255	
Tyr Asn Gln Phe Arg Arg Asp Met Thr Leu Met Val Leu Asp Leu Val			
260	265	270	
Ala Leu Phe Pro Ser Tyr Asp Thr Gln Met Tyr Pro Ile Lys Thr Thr			
275	280	285	
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His			
290	295	300	
Pro His Pro Ser Phe Thr Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro			
305	310	315	320
Ser Phe Ser Ala Ile Glu Ala Ala Val Val Arg Asn Pro His Leu Leu			
325	330	335	
Asp Phe Leu Glu Gln Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser			
340	345	350	
Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Lys Leu Glu Phe Arg			
355	360	365	
Thr Ile Gly Gly Thr Leu Asn Ile Ser Thr Gln Gly Ser Thr Asn Thr			
370	375	380	
Ser Ile Asn Pro Val Thr Leu Pro Phe Thr Ser Arg Asp Val Tyr Arg			
385	390	395	400
Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn			
405	410	415	
Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Val Thr His Pro Ile			
420	425	430	
Ala Ser Asp Asn Phe Tyr Tyr Pro Gly Tyr Ala Gly Ile Gly Thr Gln			
435	440	445	
Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Ala Thr Gly Gln Pro			
450	455	460	
Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser			
465	470	475	480
Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala			
485	490	495	
Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu			
500	505	510	
Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro			
515	520	525	
Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe			
530	535	540	
Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg			
545	550	555	560
Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser			

	565	570	575
Ile Asn Gly Lys Ala Ile Asn Gln	Gly Asn Phe Ser Ala Thr Met Asn		
580	585	590	
Arg Gly Glu Asp Leu Asp Tyr Lys	Thr Phe Arg Thr Val Gly Phe Thr		
595	600	605	
Thr Pro Phe Ser Phe Leu Asp Val	Gln Ser Thr Phe Thr Ile Gly Ala		
610	615	620	
Trp Asn Phe Ser Ser Gly Asn Glu Val	Tyr Ile Asp Arg Ile Glu Phe		
625	630	635	640
Val Pro Val Glu Val Thr Tyr Glu Ala	Glu Tyr Asp Phe Glu Lys Ala		
645	650	655	
Gln Glu Lys Val Thr Ala Leu Phe	Thr Ser Thr Asn Pro Arg Gly Leu		
660	665	670	
Lys Thr Asp Val Lys Asp Tyr His	Ile Asp Gln Val Ser Asn Leu Val		
675	680	685	
Glu Ser Leu Ser Asp Glu Phe	Tyr Leu Asp Glu Lys Arg Glu Leu Phe		
690	695	700	
Glu Ile Val Lys Tyr Ala Asn Glu	Leu His Ile Glu Arg Asn Met		
705	710	715	

<210> 59

<211> 719

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN cry1Ib1 Embl. Accession No. U07642

<400> 59

Met Lys Leu Lys Asn Pro Asp Lys His Gln Ser Leu Ser Ser Asn Ala			
1	5	10	15
Lys Val Asp Lys Ile Ala Thr Asp Ser Leu Lys Asn Glu Thr Asp Ile			
20	25	30	
Glu Leu Lys Asn Met Asn Asn Glu Asp Tyr Leu Arg Met Ser Glu His			
35	40	45	
Glu Ser Ile Asp Pro Phe Val Ser Ala Ser Thr Ile Gln Thr Gly Ile			
50	55	60	
Gly Ile Ala Gly Lys Ile Leu Gly Thr Leu Gly Val Pro Phe Ala Gly			
65	70	75	80
Gln Ile Ala Ser Leu Tyr Ser Phe Ile Leu Gly Glu Leu Trp Pro Lys			
85	90	95	
Gly Lys Ser Gln Trp Glu Ile Phe Met Glu His Val Glu Glu Ile Ile			
100	105	110	
Asn Gln Lys Ile Leu Thr Tyr Ala Arg Asn Lys Ala Leu Ser Asp Leu			
115	120	125	
Arg Gly Leu Gly Asp Ala Leu Ala Val Tyr His Glu Ser Leu Glu Ser			
130	135	140	
Trp Val Glu Asn Arg Asn Asn Thr Arg Ala Arg Ser Val Val Lys Asn			
145	150	155	160
Gln Tyr Ile Ala Leu Glu Leu Met Phe Val Gln Lys Leu Pro Ser Phe			
165	170	175	
Ala Val Ser Gly Glu Glu Val Pro Leu Leu Pro Ile Tyr Ala Gln Ala			
180	185	190	
Ala Asn Leu His Leu Leu Leu Arg Asp Ala Ser Ile Phe Gly Lys			
195	200	205	
Glu Trp Gly Leu Ser Ala Ser Glu Ile Ser Thr Phe Tyr Asn Arg Gln			
210	215	220	
Val Glu Arg Thr Arg Asp Tyr Ser Asp His Cys Ile Lys Trp Tyr Asn			
225	230	235	240

Thr Gly Leu Asn Asn Leu Arg Gly Thr Asn Ala Lys Ser Trp Val Arg
 245 250 255
 Tyr Asn Gln Phe Arg Lys Asp Met Thr Leu Met Val Leu Asp Leu Val
 260 265 270
 Ala Leu Phe Pro Ser Tyr Asp Thr Leu Val Tyr Pro Ile Lys Thr Thr
 275 280 285
 Ser Gln Leu Thr Arg Glu Val Tyr Thr Asp Ala Ile Gly Thr Val His
 290 295 300
 Pro Asn Gln Ala Phe Ala Ser Thr Thr Trp Tyr Asn Asn Asn Ala Pro
 305 310 315 320
 Ser Phe Ser Ala Ile Glu Ala Ala Val Ile Arg Ser Pro His Leu Leu
 325 330 335
 Asp Phe Leu Glu Lys Val Thr Ile Tyr Ser Leu Leu Ser Arg Trp Ser
 340 345 350
 Asn Thr Gln Tyr Met Asn Met Trp Gly Gly His Arg Leu Glu Ser Arg
 355 360 365
 Pro Ile Gly Gly Ala Leu Asn Thr Ser Thr Gln Gly Ser Thr Asn Thr
 370 375 380
 Ser Ile Asn Pro Val Thr Leu Gln Phe Thr Ser Arg Asp Val Tyr Arg
 385 390 395 400
 Thr Glu Ser Leu Ala Gly Leu Asn Leu Phe Leu Thr Gln Pro Val Asn
 405 410 415
 Gly Val Pro Arg Val Asp Phe His Trp Lys Phe Pro Thr Leu Pro Ile
 420 425 430
 Ala Ser Asp Asn Phe Tyr Tyr Leu Gly Tyr Ala Gly Val Gly Thr Gln
 435 440 445
 Leu Gln Asp Ser Glu Asn Glu Leu Pro Pro Glu Thr Thr Gly Gln Pro
 450 455 460
 Asn Tyr Glu Ser Tyr Ser His Arg Leu Ser His Ile Gly Leu Ile Ser
 465 470 475 480
 Ala Ser His Val Lys Ala Leu Val Tyr Ser Trp Thr His Arg Ser Ala
 485 490 495
 Asp Arg Thr Asn Thr Ile Glu Pro Asn Ser Ile Thr Gln Ile Pro Leu
 500 505 510
 Val Lys Ala Phe Asn Leu Ser Ser Gly Ala Ala Val Val Arg Gly Pro
 515 520 525
 Gly Phe Thr Gly Gly Asp Ile Leu Arg Arg Thr Asn Thr Gly Thr Phe
 530 535 540
 Gly Asp Ile Arg Val Asn Ile Asn Pro Pro Phe Ala Gln Arg Tyr Arg
 545 550 555 560
 Val Arg Ile Arg Tyr Ala Ser Thr Thr Asp Leu Gln Phe His Thr Ser
 565 570 575
 Ile Asn Gly Lys Ala Ile Asn Gln Gly Asn Phe Ser Ala Thr Met Asn
 580 585 590
 Arg Gly Glu Asp Leu Asp Tyr Lys Thr Phe Arg Thr Ile Gly Phe Thr
 595 600 605
 Thr Pro Phe Ser Phe Ser Asp Val Gln Ser Thr Phe Thr Ile Gly Ala
 610 615 620
 Trp Asn Phe Ser Ser Gly Asn Glu Val Tyr Ile Asp Arg Ile Glu Phe
 625 630 635 640
 Val Pro Val Glu Val Thr Tyr Glu Ala Glu Tyr Asp Phe Glu Lys Ala
 645 650 655
 Gln Glu Lys Val Thr Ala Leu Phe Thr Ser Thr Asn Pro Arg Gly Leu
 660 665 670
 Lys Thr Asp Val Lys Asp Tyr His Ile Asp Gln Val Ser Asn Leu Val
 675 680 685
 Glu Ser Leu Ser Asp Glu Phe Tyr Leu Asp Glu Lys Arg Glu Leu Phe
 690 695 700
 Glu Ile Val Lys Tyr Ala Lys Gln Ile His Ile Glu Arg Asn Met
 705 710 715

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<210> 60
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> PROTEIN

<221> VARIANT
<222> 1, 2, 3, 5, 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 19, 20, 21,
      22, 24, 25, 26, 27, 28, 29, 30, 31, 33
<223> Xaa = Any Amino Acid

<400> 60
Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
    1           5           10          15
Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
    20          25          30
Xaa

<210> 61
<211> 439
<212> DNA
<213> Paecilomyces sp.

<400> 61
tctacttctt catctcacgc catatatcct cccaaaatca cacctttcc ttcaccatgc 60
aaatctccgc cgtcattgtc gcactctcg ccagcgccgc catggccggc aagatctgca 120
ctcctgctgg agttgtacgt atttcatcc atttcctyca ccactcctct aacatgaagc 180
aactttctct tctctctaga aatgtcccgcc ggctttccct tgctgccccg gacttcgctg 240
catcgccggc gtcaacgtaa gtcaccatgg atctggcaag cgagaccata acatgacgca 300
gtatactaac cctggccgtt atagaacaag gttgtgagtc gacatgtkt acaacctcta 360
caaacgcgcg cactaatgac aacggtagtg ccggtaattc tagtgcgca acttttgagc 420
gtgggataag tatgcttcg                                     439

<210> 62
<211> 438
<212> DNA
<213> Paecilomyces sp.

<400> 62
attacccaag tttgaggggca ttcaatttca cacagtctca cgctttcgac gcatctactt 60
cttcgtctca cgccatataat cctccaaaaa tcacacctct tccttcacca tgcaaatctc 120
cgccgtcatt gtcgcactct tcgcccagcgc cgccatggcc ggcaagatct gcactcctgc 180
tggagttaaa tgtcccgccg ctcttccttg ctgccccggc cttcgctgca tcggccggcgt 240
caacaacaag gtttgcgggt aattcttagtg tcgcaacttt tgagcgtggg ataagtatgc 300
ttcggtcggt gtatggagtt ctcctccgga gtttaagctc ggccggcgtca cagcgggtct 360
gctatacttg atcttacagc gatactattg atagaaatgc acatttcat tcatgcgtca 420
tgaaaaaaaaaaaaaaaaa                                         438

<210> 63
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

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<223> INSECTICIDAL PROTEIN MOTIF

<400> 63

Leu Pro Cys Cys Pro Gly
1 5

<210> 64

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> INSECTICIDAL PROTEIN MOTIF

<400> 64

Ile Cys Thr Pro Ala
1 5

<210> 65

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> PROTEIN REGION N-TERMINAL

<221> VARIANT

<222> 1, 2

<223> Xaa = Any Amino Acid

<400> 65

Xaa Xaa Ile Cys Thr
1 5